

SEQUENCE LISTING

<110> Curtis, Rory A.J.

<120> 52906, 33408, AND 12189, NOVEL POTASSIUM
CHANNEL FAMILY MEMBERS AND USES THEREOF

<130> 10448-061001

<150> US 60/209,845

<151> 2000-06-06

<160> 13

<170> FastSEQ for Windows Version 4.0

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<211> 3525

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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gcagccggca gccactctc ggccgggatga tctgggagaa gcgggcgtgg gacgaggggg      240
ctgctgtttt gcagccctgc gaggcgtgca gtcggagaag tggtcggggg tccacaccgt      300
ccctgagcct gccccctggc caaggtggcc cgacgtgctg cagtggctgg cgcaggtgat      360
ccgggcagcg cgtccggcac tagtcaaggg ggcagcggca cgggagggag gggcgccctt      420
ctcttttctc ctccccctgc agcccagctg cactgcgtgg gggctctcca tctccacgca      480
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cgc cca acc aat cgg act cgc cgc ctg gat tct acc gga gcc ggc atg      703
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ggc cct tcc tcg cac cag cag cag gag tcc ccg ctc ccg acc ata acg      751
Gly Pro Ser Ser His Gln Gln Gln Glu Ser Pro Leu Pro Thr Ile Thr
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cat tgc gca ggg tgc acc acc gct tgg tct ccc tgc agc ttt aac agc      799
His Cys Ala Gly Cys Thr Thr Ala Trp Ser Pro Cys Ser Phe Asn Ser
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cct gac atg gaa acc cca ttg cag ttc cag cgc ggc ttc ttc cca gag      847
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75 80 85	
caa cag agc cag gac aag ccg tgc ccg ccc ttc gcg ccc ctc ccg cac	943
Gln Gln Ser Gln Asp Lys Pro Cys Pro Pro Phe Ala Pro Leu Pro His	
90 95 100	
cct cac cac cac ccg cac ctc gcg cac cag cag ccg gcc agc ggc ggc	991
Pro His His His Pro His Leu Ala His Gln Gln Pro Ala Ser Gly Gly	
105 110 115	
agc agc cca tgc ctc cgg tgc aac agc tgc gcc tcc tcc ggt gcc ccg	1039
Ser Ser Pro Cys Leu Arg Cys Asn Ser Cys Ala Ser Ser Gly Ala Pro	
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Ala Ala Gly Ala Gly Asp Asn Leu Ser Leu Leu Leu Arg Thr Ser Ser	
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Pro Gly Gly Ala Phe Arg Thr Arg Thr Ser Ser Pro Leu Ser Gly Ser	
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tcc tgc tgc tgc tgc tgc tgc tcg tcg cgc cgg ggc agc cag ctc aat	1183
Ser Cys Cys Cys Cys Cys Cys Ser Ser Arg Arg Gly Ser Gln Leu Asn	
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gtg agc gag ctg acg ccg tcc agc cat gcc agt gcg ctc cgg cag cag	1231
Val Ser Glu Leu Thr Pro Ser Ser His Ala Ser Ala Leu Arg Gln Gln	
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Tyr Ala Gln Gln Ser Ala Gln Gln Ser Ala Ser Ala Ser Gln Tyr His	
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cag tgc cac agc ctg cag ccc gcc gcc agc ccc acg ggc agc ctc ggc	1327
Gln Cys His Ser Leu Gln Pro Ala Ala Ser Pro Thr Gly Ser Leu Gly	
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agt ctg ggc tcc ggg ccc ccg ctc tcg cac cac cac cac cac ccg cac	1375
Ser Leu Gly Ser Gly Pro Pro Leu Ser His His His His His Pro His	
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ccg gcg cac cac cag cac cac cag ccc cag gcg cgc cgc gag agc aac	1423
Pro Ala His His Gln His His Gln Pro Gln Ala Arg Arg Glu Ser Asn	
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ccc ttc acc gaa ata gcc atg agc agc tgc agg tac aac ggg ggc gtc	1471
Pro Phe Thr Glu Ile Ala Met Ser Ser Cys Arg Tyr Asn Gly Gly Val	
265 270 275	
atg cgg ccg ctc agc aac ttg agc gcg tcc cgc cgg aac ctg cac gag	1519
Met Arg Pro Leu Ser Asn Leu Ser Ala Ser Arg Arg Asn Leu His Glu	
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ggg ggc ggc gcg tcc tcc ccg tct gca gcc gct gcc gcc gcc gcc gct	1615
Gly Gly Gly Ala Ser Ser Pro Ser Ala Ala Ala Ala Ala Ala Ala	
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gtt tcg tcc tca gcc ccc gag atc gtg gtg tct aag ccc gag cac aac	1663
Val Ser Ser Ser Ala Pro Glu Ile Val Val Ser Lys Pro Glu His Asn	
330 335 340	
aac tcc aac aac ctg gcg ctc tat gga acc ggc ggc gga ggc agc act	1711
Asn Ser Asn Asn Leu Ala Leu Tyr Gly Thr Gly Gly Gly Gly Ser Thr	
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Gly Gly Gly Gly Gly Gly Gly Gly Ser Gly His Gly Ser Ser Ser Gly	
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acc aag tcc agc aaa aag aaa aac cag aac atc ggc tac aag ctg ggc	1807
Thr Lys Ser Ser Lys Lys Lys Asn Gln Asn Ile Gly Tyr Lys Leu Gly	
375 380 385 390	
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His Arg Arg Ala Leu Phe Glu Lys Arg Lys Arg Leu Ser Asp Tyr Ala	
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Leu Ile Phe Gly Met Phe Gly Ile Val Val Met Val Ile Glu Thr Glu	
410 415 420	
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Leu Ser Trp Gly Ala Tyr Asp Lys Ala Ser Leu Tyr Ser Leu Ala Leu	
425 430 435	
aaa tgc ctt atc agt ctc tcc acg atc atc ctg ctc ggt ctg atc atc	1999
Lys Cys Leu Ile Ser Leu Ser Thr Ile Ile Leu Leu Gly Leu Ile Ile	
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Leu Glu Ile Leu Val Cys Ala Ile His Pro Ile Pro Gly Asn Tyr Thr	
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Phe Thr Trp Thr Ala Arg Leu Ala Phe Ser Tyr Ala Pro Ser Thr Thr	
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Tyr	Leu	Ile	Ala	Arg	Val	Met	Leu	Leu	His	Ser	Lys	Leu	Phe	Thr	Asp		
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Arg	Phe	Val	Met	Lys	Thr	Leu	Met	Thr	Ile	Cys	Pro	Gly	Thr	Val	Leu		
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Leu	Val	Phe	Ser	Ile	Ser	Leu	Trp	Ile	Ile	Ala	Ala	Trp	Thr	Val	Arg		
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Asp	Met	Val	Pro	Asn	Thr	Tyr	Cys	Gly	Lys	Gly	Val	Cys	Leu	Leu	Thr		
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Leu	Arg	Glu	Thr	Trp	Leu	Ile	Tyr	Lys	Asn	Thr	Lys	Leu	Val	Lys	Lys		
695					700					705					710		
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Ile	His	Gln	Leu	Arg	Ser	Val	Lys	Met	Glu	Gln	Arg	Lys	Leu	Asn	Asp		
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Ile Val Thr Leu Glu Thr Lys Leu Glu Thr Leu Ile Gly Ser Ile His			
775	780	785	790
gcc ctc cct ggg ctc ata agc cag acc atc agg cag cag cag aga gat			3055
Ala Leu Pro Gly Leu Ile Ser Gln Thr Ile Arg Gln Gln Gln Arg Asp			
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ttc att gag gct cag atg gag agc tac gac aag cac gtc act tac aat			3103
Phe Ile Glu Ala Gln Met Glu Ser Tyr Asp Lys His Val Thr Tyr Asn			
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Ala Pro Pro Thr Ser Ser Glu Ser Ser			
840	845		
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 35 40 45
 Pro Cys Ser Phe Asn Ser Pro Asp Met Glu Thr Pro Leu Gln Phe Gln
 50 55 60
 Arg Gly Phe Phe Pro Glu Gln Pro Pro Pro Pro Pro Arg Ser Ser His
 65 70 75 80
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 85 90 95
 Phe Ala Pro Leu Pro His Pro His His His Pro His Leu Ala His Gln
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 Gln Pro Ala Ser Gly Gly Ser Ser Pro Cys Leu Arg Cys Asn Ser Cys
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 Ala Ser Ser Gly Ala Pro Ala Ala Gly Ala Gly Asp Asn Leu Ser Leu
 130 135 140

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 165 170 175
 Arg Gly Ser Gln Leu Asn Val Ser Glu Leu Thr Pro Ser Ser His Ala
 180 185 190
 Ser Ala Leu Arg Gln Gln Tyr Ala Gln Gln Ser Ala Gln Gln Ser Ala
 195 200 205
 Ser Ala Ser Gln Tyr His Gln Cys His Ser Leu Gln Pro Ala Ala Ser
 210 215 220
 Pro Thr Gly Ser Leu Gly Ser Leu Gly Ser Gly Pro Pro Leu Ser His
 225 230 235 240
 His His His His Pro His Pro Ala His His Gln His His Gln Pro Gln
 245 250 255
 Ala Arg Arg Glu Ser Asn Pro Phe Thr Glu Ile Ala Met Ser Ser Cys
 260 265 270
 Arg Tyr Asn Gly Gly Val Met Arg Pro Leu Ser Asn Leu Ser Ala Ser
 275 280 285
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 Pro Ala Ser Val Gly Gly Gly Gly Gly Ala Ser Ser Pro Ser Ala Ala
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 325 330 335
 Ser Lys Pro Glu His Asn Asn Ser Asn Asn Leu Ala Leu Tyr Gly Thr
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 355 360 365
 His Gly Ser Ser Ser Gly Thr Lys Ser Ser Lys Lys Lys Asn Gln Asn
 370 375 380
 Ile Gly Tyr Lys Leu Gly His Arg Arg Ala Leu Phe Glu Lys Arg Lys
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 405 410 415
 Met Val Ile Glu Thr Glu Leu Ser Trp Gly Ala Tyr Asp Lys Ala Ser
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 Ile Pro Gly Asn Tyr Thr Phe Thr Trp Thr Ala Arg Leu Ala Phe Ser
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His Val His Asn Phe Met Met Asp Thr Gln Leu Thr Lys Arg Val Lys		
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Asn Ala Ala Ala Asn Val Leu Arg Glu Thr Trp Leu Ile Tyr Lys Asn		
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Thr Lys Leu Val Lys Lys Ile Asp His Ala Lys Val Arg Lys His Gln		
705	710	715
Arg Lys Phe Leu Gln Ala Ile His Gln Leu Arg Ser Val Lys Met Glu		
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Gln Arg Lys Leu Asn Asp Gln Ala Asn Thr Leu Val Asp Leu Ala Lys		
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Leu Ile Gly Ser Ile His Ala Leu Pro Gly Leu Ile Ser Gln Thr Ile		
785	790	795
Arg Gln Gln Gln Arg Asp Phe Ile Glu Ala Gln Met Glu Ser Tyr Asp		
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Pro Val Val Tyr Ser Asn Asp Gly Phe Cys Lys Leu Ser Gly Tyr His
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Glu Leu Thr Asp Lys Lys Thr Ile Glu Lys Val Arg Gln Thr Phe Asp				
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aac tac gaa tca aac tgc ttt gaa gtt ctt ctg tac aag aaa aac aga				583
Asn Tyr Glu Ser Asn Cys Phe Glu Val Leu Leu Tyr Lys Lys Asn Arg				
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acc cct gtt tgg ttt tat atg caa att gca cca ata aga aat gaa cat				631
Thr Pro Val Trp Phe Tyr Met Gln Ile Ala Pro Ile Arg Asn Glu His				
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Glu Lys Val Val Leu Phe Leu Cys Thr Phe Lys Asp Ile Thr Leu Phe				
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Lys Gln Pro Ile Glu Asp Asp Ser Thr Lys Gly Trp Thr Lys Phe Ala				
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Thr Pro Met Asn Lys Thr Glu Val His Lys His Ser Arg Leu Ala				
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Glu Val Leu Gln Leu Gly Ser Asp Ile Leu Pro Gln Tyr Lys Gln Glu				
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Ala Pro Lys Thr Pro Pro His Ile Ile Leu His Tyr Cys Ala Phe Lys				
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Thr Thr Trp Asp Trp Val Ile Leu Ile Leu Thr Phe Tyr Thr Ala Ile				
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Trp Leu Val Leu Asp Ser Val Val Asp Val Ile Phe Leu Val Asp Ile				
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gtt tta aat ttt cac acg act ttc gtg ggg ccc ggt gga gag gtc att				1111
Val Leu Asn Phe His Thr Thr Phe Val Gly Pro Gly Gly Glu Val Ile				
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Ser Asp Pro Lys Leu Ile Arg Met Asn Tyr Leu Lys Thr Trp Phe Val				
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Asn Val Asp Glu Gly Ile Ser Ser Leu Phe Ser Ser Leu Lys Val Val	
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Arg Leu Leu Arg Leu Gly Arg Val Ala Arg Lys Leu Asp His Tyr Leu	
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Val Ile Asp Glu Val Thr Asn Thr Ile Gln Ile Asp Ser Trp Leu Tyr	
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Asn Val Arg Asp Phe Leu Lys Leu Tyr Gln Val Pro Lys Gly Leu Ser	
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Glu Arg Val Met Asp Tyr Ile Val Ser Thr Trp Ser Met Ser Lys Gly	
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Asp Ile Cys Val His Leu Asn Arg Lys Val Phe Asn Glu His Pro Ala	
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Phe Arg Leu Ala Ser Asp Gly Cys Leu Arg Ala Leu Ala Val Glu Phe	
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Ser Val Asp Ala Leu Cys Phe Val Val Ser Gly Ser Leu Glu Val Ile	
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970

975

980

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Tyr	His	Glu	Met	Leu	Asn	Asn	Val	Arg	Asp	Phe	Leu	Lys	Leu	Tyr	Gln
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gatgtgaaga aagaggagga ggagcgctc atgaggtgac cctcagcatt 2100
cccgtggacc acccagtcag aaagctcttc cagaagttca agcagcagaa ggagctgcgg 2160
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ataagaatga agaattgaaa tggaaaaggg tggctgcgac tcaagaataa tatgggagcc 2460
catgaggaga aaaaggaaga ctggaataat gtcactaaag ctgagtcaat ggggctattg 2520
tctgaggacc ccaagagcag tgattcagag aacagtgtga ccaaaaaccc actaaggaaa 2580
acagattcct gtgacagtgg aattacaaaa agtgaccttc gtttggataa ggctggggag 2640
gcccgaagtc cgctagagca cagtcccatc caggctgatg ccaagcacc cttttatccc 2700
atccccgagc aggccttaca gaccacactg caggaagtca aacacgaact caaagaggac 2760
atccagctgc tcagctgcag aatgactgcc ctagaaaagc aggtggcaga aattttaaaa 2820
atactgtcgg aaaaaagcgt accccaggcc tcatctccca aatcccaat gccactccaa 2880
gtaccccccc agataccatg tcaggatatt tttagtgtct caaggcctga atcacctgaa 2940
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<210> 7

<211> 1341

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1338)

<400> 7

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tgc tgc gag cgg ctg gtg ctc aac gtg gcc ggg ctg cgc ttc gag acg 48
Cys Cys Glu Arg Leu Val Leu Asn Val Ala Gly Leu Arg Phe Glu Thr
1 5 10 15

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cgg gcg cgc acg ctg ggc cgc ttc ccg gac act ctg cta ggg gac cca 96
Arg Ala Arg Thr Leu Gly Arg Phe Pro Asp Thr Leu Leu Gly Asp Pro
20 25 30

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gcg cgc cgc ggc cgc ttc tac gac gac gcg cgc cgc gag tat ttc ttc 144
Ala Arg Arg Gly Arg Phe Tyr Asp Asp Ala Arg Arg Glu Tyr Phe Phe
35 40 45

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gac cgg cac cgg ccc agc ttc gac gcc gtg ctc tac tac tac cag tcc 192
Asp Arg His Arg Pro Ser Phe Asp Ala Val Leu Tyr Tyr Tyr Gln Ser
50 55 60

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ggg ggg cgg ctg cgg cgg ccg gcg cac gtg ccg ctc gac gtc ttc ctg 240
Gly Gly Arg Leu Arg Arg Pro Ala His Val Pro Leu Asp Val Phe Leu

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65	70	75	80	
gaa gag gtg gcc ttc tac ggg ctg ggc gcg gcg gcc ctg gca cgc ctg				288
Glu Glu Val Ala Phe Tyr Gly Leu Gly Ala Ala Ala Leu Ala Arg Leu	85	90	95	
cgc gag gac gag ggc tgc ccg gtg ccg ccc gag cgc ccc ctg ccc cgc				336
Arg Glu Asp Glu Gly Cys Pro Val Pro Pro Glu Arg Pro Leu Pro Arg	100	105	110	
cgc gcc ttc gcc cgc cag ctg tgc ctg ctt ttc gag ttt ccc gag agc				384
Arg Ala Phe Ala Arg Gln Leu Cys Leu Leu Phe Glu Phe Pro Glu Ser	115	120	125	
tct cag gcc gcg cgc gtg ctc gcc gta gtc tcc gtg ctg gtc atc ctc				432
Ser Gln Ala Ala Arg Val Leu Ala Val Val Ser Val Leu Val Ile Leu	130	135	140	
gtc tcc atc gtc gtc ttc tgc ctc gag acg ctg cct gac ttc cgc gac				480
Val Ser Ile Val Val Phe Cys Leu Glu Thr Leu Pro Asp Phe Arg Asp	145	150	155	160
gac cgc gac ggc acg ggg ctt gct gct gca gcc gca gcc ggc ccg ttc				528
Asp Arg Asp Gly Thr Gly Leu Ala Ala Ala Ala Ala Ala Gly Pro Phe	165	170	175	
ccc gct ccg ctg aat ggc tcc agc caa atg cct gga aat cca ccc cgc				576
Pro Ala Pro Leu Asn Gly Ser Ser Gln Met Pro Gly Asn Pro Pro Arg	180	185	190	
ctg ccc ttc aat gac ccg ttc ttc gtg gtg gag acg ctg tgt att tgt				624
Leu Pro Phe Asn Asp Pro Phe Phe Val Val Glu Thr Leu Cys Ile Cys	195	200	205	
tgg ttc tcc ttt gag ctg ctg gta cgc ctc ctg gtc tgt cca agc aag				672
Trp Phe Ser Phe Glu Leu Leu Val Arg Leu Leu Val Cys Pro Ser Lys	210	215	220	
gct atc ttc ttc aag aac gtg atg aac ctc atc gat ttt gtg gct atc				720
Ala Ile Phe Phe Lys Asn Val Met Asn Leu Ile Asp Phe Val Ala Ile	225	230	235	240
ctt ccc tac ttt gtg gca ctg ggc acc gag ctg gcc cgg cag cga ggg				768
Leu Pro Tyr Phe Val Ala Leu Gly Thr Glu Leu Ala Arg Gln Arg Gly	245	250	255	
gtg ggc cag cag gcc atg tca ctg gcc atc ctg aga gtc atc cga ttg				816
Val Gly Gln Gln Ala Met Ser Leu Ala Ile Leu Arg Val Ile Arg Leu	260	265	270	
gtg cgt gtc ttc cgc atc ttc aag ctg tcc cgg cac tca aag ggc ctg				864
Val Arg Val Phe Arg Ile Phe Lys Leu Ser Arg His Ser Lys Gly Leu	275	280	285	
caa atc ttg ggc cag acg ctt cgg gcc tcc atg cgt gag ctg ggc ctc				912
Gln Ile Leu Gly Gln Thr Leu Arg Ala Ser Met Arg Glu Leu Gly Leu	290	295	300	

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ctc atc ttt ttc ctc ttc atc ggt gtg gtc ctc ttt tcc agc gcc gtc 960
 Leu Ile Phe Phe Leu Phe Ile Gly Val Val Leu Phe Ser Ser Ala Val
 305 310 315 320

tac ttt gcc gaa gtt gac cgg gtg gac tcc cat ttc act agc atc cct 1008
 Tyr Phe Ala Glu Val Asp Arg Val Asp Ser His Phe Thr Ser Ile Pro
 325 330 335

gag tcc ttc tgg tgg gcg gta gtc acc atg act aca gtt ggc tat gga 1056
 Glu Ser Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly Tyr Gly
 340 345 350

gac atg gca ccc gtc act gtg ggt ggc aag ata gtg ggc tct ctg tgt 1104
 Asp Met Ala Pro Val Thr Val Gly Gly Lys Ile Val Gly Ser Leu Cys
 355 360 365

gcc att gcg ggc gtg ctg act att tcc ctg cca gtg ccc gtc att gtc 1152
 Ala Ile Ala Gly Val Leu Thr Ile Ser Leu Pro Val Pro Val Ile Val
 370 375 380

tcc aat ttc agc tac ttt tat cac cgg gag aca gag ggc gaa gag gct 1200
 Ser Asn Phe Ser Tyr Phe Tyr His Arg Glu Thr Glu Gly Glu Glu Ala
 385 390 395 400

ggg atg ttc agc cat gtg gac atg cag cct tgt ggc cca ctg gag ggc 1248
 Gly Met Phe Ser His Val Asp Met Gln Pro Cys Gly Pro Leu Glu Gly
 405 410 415

aag gcc aat ggg ggg ctg gtg gac ggg gag gta cct gag cta cca cct 1296
 Lys Ala Asn Gly Gly Leu Val Asp Gly Glu Val Pro Glu Leu Pro Pro
 420 425 430

cca ctc tgg gca ccc cca ggg aaa cac ctg gtc acc gaa gtg 1338
 Pro Leu Trp Ala Pro Pro Gly Lys His Leu Val Thr Glu Val
 435 440 445

tga 1341

<210> 8

<211> 446

<212> PRT

<213> Homo sapiens

<400> 8

Cys Cys Glu Arg Leu Val Leu Asn Val Ala Gly Leu Arg Phe Glu Thr
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 Arg Ala Arg Thr Leu Gly Arg Phe Pro Asp Thr Leu Leu Gly Asp Pro
 20 25 30
 Ala Arg Arg Gly Arg Phe Tyr Asp Asp Ala Arg Arg Glu Tyr Phe Phe
 35 40 45
 Asp Arg His Arg Pro Ser Phe Asp Ala Val Leu Tyr Tyr Tyr Gln Ser
 50 55 60
 Gly Gly Arg Leu Arg Arg Pro Ala His Val Pro Leu Asp Val Phe Leu
 65 70 75 80
 Glu Glu Val Ala Phe Tyr Gly Leu Gly Ala Ala Ala Leu Ala Arg Leu
 85 90 95

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Arg Glu Asp Glu Gly Cys Pro Val Pro Pro Glu Arg Pro Leu Pro Arg
 100 105 110
 Arg Ala Phe Ala Arg Gln Leu Cys Leu Leu Phe Glu Phe Pro Glu Ser
 115 120 125
 Ser Gln Ala Ala Arg Val Leu Ala Val Val Ser Val Leu Val Ile Leu
 130 135 140
 Val Ser Ile Val Val Phe Cys Leu Glu Thr Leu Pro Asp Phe Arg Asp
 145 150 155 160
 Asp Arg Asp Gly Thr Gly Leu Ala Ala Ala Ala Gly Pro Phe
 165 170 175
 Pro Ala Pro Leu Asn Gly Ser Ser Gln Met Pro Gly Asn Pro Pro Arg
 180 185 190
 Leu Pro Phe Asn Asp Pro Phe Phe Val Val Glu Thr Leu Cys Ile Cys
 195 200 205
 Trp Phe Ser Phe Glu Leu Leu Val Arg Leu Leu Val Cys Pro Ser Lys
 210 215 220
 Ala Ile Phe Phe Lys Asn Val Met Asn Leu Ile Asp Phe Val Ala Ile
 225 230 235 240
 Leu Pro Tyr Phe Val Ala Leu Gly Thr Glu Leu Ala Arg Gln Arg Gly
 245 250 255
 Val Gly Gln Gln Ala Met Ser Leu Ala Ile Leu Arg Val Ile Arg Leu
 260 265 270
 Val Arg Val Phe Arg Ile Phe Lys Leu Ser Arg His Ser Lys Gly Leu
 275 280 285
 Gln Ile Leu Gly Gln Thr Leu Arg Ala Ser Met Arg Glu Leu Gly Leu
 290 295 300
 Leu Ile Phe Phe Leu Phe Ile Gly Val Val Leu Phe Ser Ser Ala Val
 305 310 315 320
 Tyr Phe Ala Glu Val Asp Arg Val Asp Ser His Phe Thr Ser Ile Pro
 325 330 335
 Glu Ser Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly Tyr Gly
 340 345 350
 Asp Met Ala Pro Val Thr Val Gly Gly Lys Ile Val Gly Ser Leu Cys
 355 360 365
 Ala Ile Ala Gly Val Leu Thr Ile Ser Leu Pro Val Pro Val Ile Val
 370 375 380
 Ser Asn Phe Ser Tyr Phe Tyr His Arg Glu Thr Glu Gly Glu Glu Ala
 385 390 395 400
 Gly Met Phe Ser His Val Asp Met Gln Pro Cys Gly Pro Leu Glu Gly
 405 410 415
 Lys Ala Asn Gly Gly Leu Val Asp Gly Glu Val Pro Glu Leu Pro Pro
 420 425 430
 Pro Leu Trp Ala Pro Pro Gly Lys His Leu Val Thr Glu Val
 435 440 445

<210> 9

<211> 223

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 9

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 1 5 10 15
 Ile Val Leu Lys Phe Ile Ala Tyr Gly Leu Lys Ser Thr Ser Asn Ile

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20 25 30
 Ala Ala Lys Tyr Leu Lys Ser Ile Phe Asn Ile Leu Asp Leu Leu Ala
 35 40 45
 Ile Leu Pro Leu Leu Leu Leu Val Leu Phe Leu Ser Gly Thr Glu
 50 55 60
 Gln Val Ala Lys Lys Arg Leu Arg Glu Arg Phe Ser Leu Glu Leu Ser
 65 70 75 80
 Gln Trp Tyr Tyr Arg Ile Leu Arg Phe Leu Arg Leu Leu Arg Leu Leu
 85 90 95
 Arg Leu Leu Arg Leu Leu Arg Leu Leu Arg Arg Leu Glu Thr Leu Phe
 100 105 110
 Glu Phe Glu Leu Gly Thr Leu Ala Trp Ser Leu Gln Ser Leu Gly Arg
 115 120 125
 Ala Leu Lys Ser Ile Leu Arg Phe Leu Leu Leu Leu Leu Leu Leu
 130 135 140
 Ile Gly Phe Ser Val Ile Gly Tyr Leu Leu Phe Lys Gly Tyr Glu Asp
 145 150 155 160
 Leu Ser Glu Asn Glu Val Asp Gly Asn Ser Glu Phe Ser Ser Tyr Phe
 165 170 175
 Asp Ala Phe Tyr Phe Leu Phe Val Thr Leu Thr Thr Val Gly Phe Gly
 180 185 190
 Asp Leu Val Pro Val Trp Leu Gly Ile Ile Phe Phe Val Leu Phe Phe
 195 200 205
 Ile Ile Val Gly Leu Leu Leu Leu Asn Leu Leu Ile Ala Val Ile
 210 215 220

<210> 10

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 10

Ala Leu Glu Glu Arg Ser Tyr Pro Ala Gly Glu Val Ile Ile Arg Gln
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 Gly Asp Pro Gly Asp Ser Phe Tyr Ile Val Leu Ser Gly Glu Val Glu
 20 25 30
 Val Tyr Lys Leu Thr Glu Asp Gly Ala Arg Thr Pro Glu Val Ser Gln
 35 40 45
 Lys Gln Asp Thr Arg Glu Gln Val Val Ala Thr Leu Gly Pro Gly Asp
 50 55 60
 Phe Phe Gly Glu Leu Ala Leu Leu Thr Asn Asp Gly Asn Lys Asn Ala
 65 70 75 80
 Val Leu Pro Ser Leu Asp Gln Gly Ala Pro Arg Thr Ala Thr Val Arg
 85 90 95
 Ala Leu Thr Asp Ser Glu Leu Leu Arg Leu Asp Arg Glu Asp Phe Arg
 100 105 110
 Arg Leu Leu Gln Lys Tyr Pro Glu
 115 120

<210> 11

<211> 111

<212> PRT

<213> Artificial Sequence

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<220>

<223> consensus sequence

<400> 11

Glu	Arg	Val	Arg	Leu	Asn	Val	Gly	Gly	Lys	Arg	Phe	Glu	Thr	Ser	Lys
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Ser	Thr	Leu	Thr	Arg	Phe	Lys	Pro	Asp	Thr	Leu	Leu	Gly	Arg	Leu	Leu
			20					25					30		
Lys	Thr	Asp	Ser	Asp	Val	His	Glu	Ala	Arg	Leu	Arg	Leu	Cys	Asp	Phe
		35					40					45			
Tyr	Asp	Asp	Glu	Thr	Gly	Glu	Tyr	Phe	Phe	Asp	Arg	Ser	Pro	Lys	His
	50					55				60					
Phe	Glu	Thr	Ile	Leu	Asn	Phe	Tyr	Arg	Thr	Gly	Asp	Gly	Lys	Leu	His
65					70					75					80
Arg	Pro	Glu	Val	Cys	Leu	Asp	Ser	Phe	Leu	Glu	Glu	Leu	Glu	Phe	Tyr
				85					90					95	
Gly	Leu	Asp	Glu	Leu	Ala	Ile	Glu	Ser	Cys	Cys	Glu	Asp	Glu	Tyr	
			100					105					110		

<210> 12

<211> 988

<212> PRT

<213> Rattus norvegicus

<400> 12

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Glu	Asn	Ile	Val	Arg	Arg	Ser	Ser	Glu	Ser	Ser	Phe	Leu	Leu	Gly	Asn
			20					25					30		
Ala	Gln	Ile	Val	Asp	Trp	Pro	Val	Val	Tyr	Ser	Asn	Asp	Gly	Phe	Cys
		35					40					45			
Lys	Leu	Ser	Gly	Tyr	His	Arg	Ala	Asp	Val	Met	Gln	Lys	Ser	Ser	Thr
	50					55				60					
Cys	Ser	Phe	Met	Tyr	Gly	Glu	Leu	Thr	Asp	Lys	Lys	Thr	Ile	Glu	Lys
65					70					75					80
Val	Arg	Gln	Thr	Phe	Asp	Asn	Tyr	Glu	Ser	Asn	Cys	Phe	Glu	Val	Leu
				85					90					95	
Leu	Tyr	Lys	Lys	Asn	Arg	Thr	Pro	Val	Trp	Phe	Tyr	Met	Gln	Ile	Ala
			100					105					110		
Pro	Ile	Arg	Asn	Glu	His	Glu	Lys	Val	Val	Leu	Phe	Leu	Cys	Thr	Phe
	115						120					125			
Lys	Asp	Ile	Thr	Leu	Phe	Lys	Gln	Pro	Ile	Glu	Asp	Asp	Ser	Thr	Lys
	130					135					140				
Gly	Trp	Thr	Lys	Phe	Ala	Arg	Leu	Thr	Arg	Ala	Leu	Thr	Asn	Ser	Arg
145					150					155					160
Ser	Val	Leu	Gln	Gln	Leu	Thr	Pro	Met	Asn	Lys	Thr	Glu	Thr	Val	His
			165						170					175	
Lys	His	Ser	Arg	Leu	Ala	Glu	Val	Leu	Gln	Leu	Gly	Ser	Asp	Ile	Leu
			180					185					190		
Pro	Gln	Tyr	Lys	Gln	Glu	Ala	Pro	Lys	Thr	Pro	Pro	His	Ile	Ile	Leu
	195						200					205			
His	Tyr	Cys	Ala	Phe	Lys	Thr	Thr	Trp	Asp	Trp	Val	Ile	Leu	Ile	Leu
	210					215					220				
Thr	Phe	Tyr	Thr	Ala	Ile	Met	Val	Pro	Tyr	Asn	Val	Ser	Phe	Lys	Thr
225					230					235					240
Lys	Gln	Asn	Asn	Ile	Ala	Trp	Leu	Val	Leu	Asp	Ser	Val	Val	Asp	Val
				245					250					255	

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Ile	Phe	Leu	Val	Asp	Ile	Val	Leu	Asn	Phe	His	Thr	Thr	Phe	Val	Gly
			260					265					270		
Pro	Gly	Gly	Glu	Val	Ile	Ser	Asp	Pro	Lys	Leu	Ile	Arg	Met	Asn	Tyr
		275					280					285			
Leu	Lys	Thr	Trp	Phe	Val	Ile	Asp	Leu	Leu	Ser	Cys	Leu	Pro	Tyr	Asp
	290					295					300				
Ile	Ile	Asn	Ala	Phe	Glu	Asn	Val	Asp	Glu	Gly	Ile	Ser	Ser	Leu	Phe
305					310					315					320
Ser	Ser	Leu	Lys	Val	Val	Arg	Leu	Leu	Arg	Leu	Gly	Arg	Val	Ala	Arg
			325						330					335	
Lys	Leu	Asp	His	Tyr	Leu	Glu	Tyr	Gly	Ala	Ala	Val	Leu	Val	Leu	Leu
			340					345					350		
Val	Cys	Val	Phe	Gly	Leu	Val	Ala	His	Trp	Leu	Ala	Cys	Ile	Trp	Tyr
		355					360					365			
Ser	Ile	Gly	Asp	Tyr	Glu	Val	Ile	Asp	Glu	Val	Thr	Asn	Thr	Ile	Gln
	370					375					380				
Ile	Asp	Ser	Trp	Leu	Tyr	Gln	Leu	Ala	Leu	Ser	Ile	Arg	Thr	Pro	Tyr
385					390					395					400
Arg	Tyr	Asn	Thr	Ser	Ala	Gly	Ile	Trp	Glu	Gly	Gly	Pro	Ser	Lys	Asp
			405						410					415	
Ser	Leu	Tyr	Val	Ser	Ser	Leu	Tyr	Phe	Thr	Met	Thr	Ser	Leu	Thr	Thr
			420					425					430		
Ile	Gly	Phe	Gly	Asn	Ile	Ala	Pro	Thr	Thr	Asp	Val	Glu	Lys	Met	Phe
		435					440					445			
Ser	Val	Ala	Met	Met	Met	Val	Gly	Ser	Leu	Leu	Tyr	Ala	Thr	Ile	Phe
	450					455					460				
Gly	Asn	Val	Thr	Thr	Ile	Phe	Gln	Gln	Met	Tyr	Ala	Asn	Thr	Asn	Arg
465					470					475					480
Tyr	His	Glu	Met	Leu	Asn	Asn	Val	Arg	Asp	Phe	Leu	Lys	Leu	Tyr	Gln
			485						490					495	
Val	Pro	Lys	Gly	Leu	Ser	Glu	Arg	Val	Met	Asp	Tyr	Ile	Val	Ser	Thr
			500					505					510		
Trp	Ser	Met	Ser	Lys	Gly	Ile	Asp	Thr	Glu	Lys	Val	Leu	Ser	Ile	Cys
		515					520					525			
Pro	Lys	Asp	Met	Arg	Ala	Asp	Ile	Cys	Val	His	Leu	Asn	Arg	Lys	Val
	530					535					540				
Phe	Asn	Glu	His	Pro	Ala	Phe	Arg	Leu	Ala	Ser	Asp	Gly	Cys	Leu	Arg
545					550					555					560
Ala	Leu	Ala	Val	Glu	Phe	Gln	Thr	Ile	His	Cys	Ala	Pro	Gly	Asp	Leu
			565						570					575	
Ile	Tyr	His	Ala	Gly	Glu	Ser	Val	Asp	Ala	Leu	Cys	Phe	Val	Val	Ser
		580						585					590		
Gly	Ser	Leu	Glu	Val	Ile	Gln	Asp	Glu	Glu	Val	Val	Ala	Ile	Leu	Gly
	595						600					605			
Lys	Gly	Asp	Val	Phe	Gly	Asp	Ile	Phe	Trp	Lys	Glu	Thr	Thr	Leu	Ala
	610					615					620				
His	Ala	Cys	Ala	Asn	Val	Arg	Ala	Leu	Thr	Tyr	Cys	Asp	Leu	His	Ile
625				630						635					640
Ile	Lys	Arg	Glu	Ala	Leu	Leu	Lys	Val	Leu	Asp	Phe	Tyr	Thr	Ala	Phe
			645						650					655	
Ala	Asn	Ser	Phe	Ser	Arg	Asn	Leu	Thr	Leu	Thr	Cys	Asn	Leu	Arg	Lys
		660						665				670			
Arg	Ile	Ile	Phe	Arg	Lys	Ile	Ser	Asp	Val	Lys	Lys	Glu	Glu	Glu	Glu
	675						680					685			
Arg	Leu	Arg	Gln	Lys	Asn	Glu	Val	Thr	Leu	Ser	Ile	Pro	Val	Asp	His
	690					695					700				
Pro	Val	Arg	Lys	Leu	Phe	Gln	Lys	Phe	Lys	Gln	Gln	Lys	Glu	Leu	Arg

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705					710					715					720
Asn	Gln	Gly	Ser	Ala	Gln	Ser	Asp	Pro	Glu	Arg	Ser	Gln	Leu	Gln	Val
				725					730					735	
Glu	Ser	Arg	Pro	Leu	Gln	Asn	Gly	Ala	Ser	Ile	Thr	Gly	Thr	Ser	Val
			740					745					750		
Val	Thr	Val	Ser	Gln	Ile	Thr	Pro	Ile	Gln	Thr	Ser	Leu	Ala	Tyr	Val
		755					760					765			
Lys	Thr	Ser	Glu	Thr	Leu	Lys	Gln	Asn	Asn	Arg	Asp	Ala	Met	Glu	Leu
	770					775					780				
Lys	Pro	Asn	Gly	Gly	Ala	Glu	Pro	Lys	Cys	Leu	Lys	Val	Asn	Ser	Pro
785					790					795					800
Ile	Arg	Met	Lys	Asn	Gly	Asn	Gly	Lys	Gly	Trp	Leu	Arg	Leu	Lys	Asn
			805						810					815	
Asn	Met	Gly	Ala	His	Glu	Glu	Lys	Lys	Glu	Glu	Trp	Asn	Asn	Val	Thr
			820						825					830	
Lys	Ala	Glu	Ser	Met	Gly	Leu	Leu	Ser	Glu	Asp	Pro	Lys	Gly	Ser	Asp
		835					840					845			
Ser	Glu	Asn	Ser	Val	Thr	Lys	Asn	Pro	Leu	Arg	Lys	Thr	Asp	Ser	Cys
	850					855					860				
Asp	Ser	Gly	Ile	Thr	Lys	Ser	Asp	Leu	Arg	Leu	Asp	Lys	Ala	Gly	Glu
865					870					875					880
Ala	Arg	Ser	Pro	Leu	Glu	His	Ser	Pro	Ser	Gln	Ala	Asp	Ala	Lys	His
			885						890					895	
Pro	Phe	Tyr	Pro	Ile	Pro	Glu	Gln	Ala	Leu	Gln	Thr	Thr	Leu	Gln	Glu
			900					905					910		
Val	Lys	His	Glu	Leu	Lys	Glu	Asp	Ile	Gln	Leu	Leu	Ser	Cys	Arg	Met
	915						920					925			
Thr	Ala	Leu	Glu	Lys	Gln	Val	Ala	Glu	Ile	Leu	Lys	Leu	Leu	Ser	Glu
	930					935					940				
Lys	Ser	Val	Pro	Gln	Thr	Ser	Ser	Pro	Lys	Pro	Gln	Ile	Pro	Leu	Gln
945					950					955					960
Val	Pro	Pro	Gln	Ile	Pro	Cys	Gln	Asp	Ile	Phe	Ser	Val	Ser	Arg	Pro
			965					970						975	
Glu	Ser	Pro	Glu	Ser	Asp	Lys	Asp	Glu	Ile	Asn	Phe				
			980					985							

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 <211> 532
 <212> PRT
 <213> Mus musculus

<400> 13
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 Ser Val Ser Thr Gly Val Gly Thr Ala Glu Gly Ala Pro Ser Pro Ala
 20 25 30
 Gly Val Thr Pro Pro Pro Pro Pro Arg Pro Gly Arg Thr Phe His Ala
 35 40 45
 Ile Phe Thr Arg Arg His Arg Thr Pro Asp Trp Gly Gly Cys Gly Val
 50 55 60
 Gly Ala Thr Arg Pro Phe Thr Gly Arg Pro Gly Cys Ala Arg His Gly
 65 70 75 80
 Ala Thr Val Pro Ala Ala Leu Arg Cys Cys Glu Arg Leu Val Leu Asn
 85 90 95
 Val Ala Gly Leu Arg Phe Glu Thr Arg Ala Arg Thr Leu Gly Arg Phe
 100 105 110
 Pro Asp Thr Leu Leu Gly Asp Pro Val Arg Arg Ser Arg Phe Tyr Asp

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